

Abstract

A method for improving the reliability and/or accuracy of physical measurements obtained from array hybridization studies performed on an array having a large number of genomic samples uses a small number of replicates insufficient for making precise and valid statistical inferences. This is overcome by estimating an error in measurement of a sample by averaging errors obtained when measuring the large number of samples or a subset of the large number of samples. The estimated sample error is utilized as a standard for accepting or rejecting the measurement of the respective sample. The samples may be independent or dependant in that correlated across two or more conditions.